UNITED STATES PATENT AND TRADEMARK OFFICE

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10/699,024	10/31/2003	Jagir Razak Jainul Abdeen Hussan	JP920030152US1	2138

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Please find below and/or attached an Office communication concerning this application or proceeding.

The time period for reply, if any, is set in the attached communication.

-- The MAILING DATE of this communication appears on the cover sheet with the correspondence address --

Period for Reply

A SHORTENED STATUTORY PERIOD FOR REPLY IS SET TO EXPIRE _3_ MONTH(S) OR THIRTY (30) DAYS, WHICHEVER IS LONGER, FROM THE MAILING DATE OF THIS COMMUNICATION.

- Extensions of time may be available under the provisions of 37 CFR 1.136(a). In no event, however, may a reply be timely filed after SIX (6) MONTHS from the mailing date of this communication.
- If NO period for reply is specified above, the maximum statutory period will apply and will expire SIX (6) MONTHS from the mailing date of this communication.
- Failure to reply within the set or extended period for reply will, by statute, cause the application to become ABANDONED (35 U.S.C. § 133). Any reply received by the Office later than three months after the mailing date of this communication, even if timely filed, may reduce any earned patent term adjustment. See 37 CFR 1.704(b).

Status

1) ☐ Responsive to communication(s) filed on _19 November 2009 and 04 November 2009_.

2a) ☐ This action is **FINAL**.   2b) ☒ This action is non-final.

3) ☐ Since this application is in condition for allowance except for formal matters, prosecution as to the merits is closed in accordance with the practice under *Ex parte Quayle*, 1935 C.D. 11, 453 O.G. 213.

Disposition of Claims

4) ☒ Claim(s) _3-6,10,14-22 and 24-28_ is/are pending in the application.

    4a) Of the above claim(s) _____ is/are withdrawn from consideration.

5) ☐ Claim(s) _____ is/are allowed.

6) ☒ Claim(s) _3-6, 10, 14-22, and 24-28_ is/are rejected.

7) ☐ Claim(s) _____ is/are objected to.

8) ☐ Claim(s) _____ are subject to restriction and/or election requirement.

Application Papers

9) ☐ The specification is objected to by the Examiner.

10) ☐ The drawing(s) filed on _____ is/are: a) ☐ accepted or b) ☐ objected to by the Examiner.

    Applicant may not request that any objection to the drawing(s) be held in abeyance. See 37 CFR 1.85(a).

    Replacement drawing sheet(s) including the correction is required if the drawing(s) is objected to. See 37 CFR 1.121(d).

11) ☐ The oath or declaration is objected to by the Examiner. Note the attached Office Action or form PTO-152.

Priority under 35 U.S.C. § 119

12) ☐ Acknowledgment is made of a claim for foreign priority under 35 U.S.C. § 119(a)-(d) or (f).

    a) ☐ All   b) ☐ Some * c) ☐ None of:

      1. ☐ Certified copies of the priority documents have been received.

      2. ☐ Certified copies of the priority documents have been received in Application No. _____.

      3. ☐ Copies of the certified copies of the priority documents have been received in this National Stage application from the International Bureau (PCT Rule 17.2(a)).

    * See the attached detailed Office action for a list of the certified copies not received.

Attachment(s)

1) ☒ Notice of References Cited (PTO-892)

2) ☐ Notice of Draftsperson's Patent Drawing Review (PTO-948)

3) ☐ Information Disclosure Statement(s) (PTO/SB/08)
    Paper No(s)/Mail Date _____.

4) ☐ Interview Summary (PTO-413)
    Paper No(s)/Mail Date. _____ .

5) ☐ Notice of Informal Patent Application

6) ☐ Other: _____.

DETAILED ACTION

Request For Continued Examination

A request for continued examination under 37 CFR 1.114, including the fee set forth in 37 CFR 1.17(e), was filed in this application after final rejection. Since this application is eligible for continued examination under 37 CFR 1.114, and the fee set forth in 37 CFR 1.17(e) has been timely paid, the finality of the previous Office action has been withdrawn pursuant to 37 CFR 1.114. Applicant's submission filed on 11/04/2009 has been entered.

Arguments/Remarks

Applicant's arguments/remarks submitted in the amendment filed 11/19/2009 have been entered.

Applicant's arguments/remarks submitted in the amendment filed 11/04/2009 have been entered and fully considered. All of the following responses pertain to these arguments.

Status of Claims

Claims 3-6, 10, 14-22, 24-28 are pending and under consideration. Claims 1-2, 7-9, 11-13, and 23 are cancelled.

Withdrawn Rejections

The rejection of claims 3-6, 10, 14-22 under 35 U.S.C. 112, second paragraph, is withdrawn in view of applicant's amendments filed 11/04/2009.

Claim rejections - 35 USC § 112, 1ˢᵗ Paragraph

Claims 3-6, 14-22, 24-28 are rejected under 35 U.S.C. 112, first paragraph, as failing to comply with the written description requirement. The claims contains subject matter which was not

described in the specification in such a way as to reasonably convey to one skilled in the relevant art that the inventor, at the time the application was filed, had possession of the claimed invention.

This is a NEW MATTER rejection.

Claims 14, 24, 27, and 28 newly recite the limitation drawn to generating a first representation that is responsive to the selected one of the certain plurality of replets but not responsive to any non-selected replets" (see claims 14, 24, 27, and 28, step viii). Applicant's response filed 11/04/2009 does not point to support the limitation. No support has been found for "non-selected replets" in the specification, drawings, or claims of the application as originally filed. The specification does provide support for replets that do not match (i.e. non-matching) [See pages 7 and 9]. However, this does not provide support for "non-selected" replets as claimed. As the newly recited limitations are not supported by the originally filed claims or disclosure, the claims are rejected for reciting new matter. This rejection is necessitated by amendment.

Claim rejections - 35 USC § 112, 2nd Paragraph

The following is a quotation of the second paragraph of 35 U.S.C. 112:

> The specification shall conclude with one or more claims particularly pointing out and distinctly claiming the subject matter which the applicant regards as his invention.

Claims 3-6, 10, 14-22 are rejected under 35 U.S.C. 112, second paragraph, as being indefinite for failing to particularly point out and distinctly claim the subject matter which applicant regards as the invention. Claims that depend directly or indirectly from claim 14 are also rejected due to said dependence.

Claims 14, 24, 27, and 28 (see step vii) recites the limitation "generating a first representation of the sequence responsive to the stored backbone sequence and at least a portion of the stored match-set data…" (see step vii).

Claims 14, 24, 27, and 28 (see step viii) recites the limitation "wherein generating a first representation in step vii) is responsive to the selected one of the certain plurality of replets but not responsive to any non-selected replete...." (see step viii).

Claims 14, 24, 27, and 28 (see step x) recites the limitation "wherein the representation in step x) is responsive to the one of the replets indicated by the selection in step ix) instead of the one of the replets indicated by the selection in step viii)...." (see step x).

In each case, the recitation of the limitation "is responsive" renders the claim unclear for the following reasons. Regarding claims 14, 24, 27, and 28 (see step vii), it is unclear in what way a computer system generates a representation of a sequence that "is responsive" to a stored backbone sequence and stored match-set data. Are these two different types of data required for generating a first representation? Are they included in the representation (e.g. graphically) or not? Regarding claims 14, 24, 27, and 28 (see step viii), it is unclear in what way the claimed first representation is "responsive" to a certain plurality of replets but not responsive to any non-selected replete. Is the non-selected replete required for generating this first representation or not? Is replet or non-replet data included in the representation (e.g. graphically)? Regarding claims 14, 24, 27, and 28 (see step x), it is unclear in what way a second representation is generated that is "responsive" to the one of the replets indicated by the selection in step ix) instead of the one of the replets indicated by the selection in step viii." What specific data is required to produce the representation? What specific data is included in the representation (e.g. graphically)? The test for definiteness under 35 U.S.C. 112, second paragraph, is whether "those skilled in the art would understand what is claimed when the claim is read in light of the specification." A review of the specification does not clarify the metes and bounds of this limitation such that a person of ordinary skill in the art would understand how to avoid infringement of the above limitations [See MPEP 2173.02]. Clarification is requested via clearer claim language.

Claims 14, 24, 27, and 28 (see step vii) recite the limitation "wherein one of the subsequence is

matched by a certain plurality of the replets." It is unclear which "subsequence" these claims are referring

to, as the claim previously recite both "matched" subsequences (see step iii), and regions of "unmatched"

sequences of a backbone sequence that remain after a deletion step (see step vi), which can also be

interpreted as subsequences. Clarification is requested via clearer claim language.

Examiner's Note

In view of the amendments filed 11/04/2009, and in order to advance prosecution, the applicant is

encouraged to contact the examiner to set up a telephonic interview discuss possible claim amendments

that would serve to clarify the invention and avoid the teachings of the cited prior art.

Claim Rejections - 35 USC § 103

The following is a quotation of 35 U.S.C. 103(a) which forms the basis for all obviousness rejections set

forth in this Office action:

> (a) A patent may not be obtained though the invention is not identically disclosed or described as set
> forth in section 102 of this title, if the differences between the subject matter sought to be patented
> and the prior art are such that the subject matter as a whole would have been obvious at the time the
> invention was made to a person having ordinary skill in the art to which said subject matter pertains.
> Patentability shall not be negatived by the manner in which the invention was made.

> This application currently names joint inventors. In considering patentability of the claims under 35
> U.S.C. 103(a), the examiner presumes that the subject matter of the various claims was commonly
> owned at the time any inventions covered therein were made absent any evidence to the contrary.
> Applicant is advised of the obligation under 37 CFR 1.56 to point out the inventor and invention dates
> of each claim that was not commonly owned at the time a later invention was made in order for the
> examiner to consider the applicability of 35 U.S.C. 103(c) and potential 35 U.S.C. 102(e), (f) or (g)
> prior art under 35 U.S.C. 103(a).

Claims 4, 5, 14-22, 24, 27, and 28 are rejected under 35 U.S.C. 103(a) as being unpatentable over

Rigoutsos et al. (Bioinformatics, 1998, Vol. 14, No. 1, p. 55-67), in view of Chen et al. (Bioinformatics,

2002, Vol. 18, No. 12, p.1696-1698), in view of Orcutt et al. (Nucleic Acids Research, 1982, Vol. 10, No.

1, p. 157-174), in view of Zhang et al. (Genome Research, 1997, Vol. 7, p.649-656), and in view of UK

CROPNETT (http://ukcrop.net/agr/sequence_display_key#sequence; Published 2001, p.1-5).

The instant claims are drawn to a computer system-implemented method for storing and

presenting sequence data, comprising: i) specifying a set of replets for analysis by a computer system; ii)

for each replet in the set, comparing each replet by the computer system to a sequence for determining by

the computer system a subsequence of the sequence that matches each replet, if any; iii) generating entries

of match-set data structures by the computer system responsive to the comparing, one match-set data

structure for each replet, a match-set data structure comprising a sequence identification to identify a

subsequence where a match occurs and offset information to determine a position within the sequence

where the matching subsequence of the sequence is located, wherein the offset information comprises a

first and second position parameter, the first position parameter denoting a location in the sequence and

the second position parameter denoting an offset from the location; iv) storing the generated entries of the

match-set data structures in a computer readable memory by the computer system; v) deleting by the

computer system each matching subsequence from the sequence where it is found; vi) concatenating by

the computer system, in order, unmatched regions of sequences that remain after deleting each matching

subsequence to form and store a backbone sequence; vii) the computer system generating a first

representation of the sequence responsive to the stored backbone sequence and at least a portion of the

stored match- set data and presenting the represented sequence to a user of the computer system; wherein

one of the subsequences is matched by a certain plurality of the replets and the method further includes:

viii) the computer system generating or receiving a selection of one of the certain plurality of replets,

wherein generating the first representation in step vii) is responsive to the selected one of the certain

plurality of replets but not responsive to any non-selected replet, and wherein the selected one of the

replets has a position within the sequence, and wherein after receiving the selection the computer system

updates the first and second parameters for any non-selected replet associated with the selected one of the

replets, the updating being responsive to the position of the selected one of the replets; ix) the computer system generating or receiving a selection of a replet that was not selected in step viii); and x) the computer system generating and presenting a second representation of the sequence, wherein the representation in step x) is responsive to the one of the replets indicated by the selection in step ix) instead of the one of the replets indicated by the selection in step viii) and wherein the computer system performs the generating in step x) by reference to the first and second parameters for the one of the replets indicated by the selection in step ix), such that the computer system performs the generating in step x) using the position parameters updated in step viii). The instant claims are also drawn to a computer readable medium and system for performing the claimed method, as described above.

Rigoutsos teaches a computer-based program (i.e. TEIRESIAS) for discovering biological sequences [Abstract and p.56]. In particular, the program generates conventional match-set entries for replets that match subsequences in a sequence [See Table 2], as stated by applicant in the Remarks filed 11/04/2009 [page 7], which meets claim language for specifying a set of replets, comparing each replete to a sequence for determining a subsequence, and generating entries of match-set data structures. The set of generated replets includes sequence identification and offset information [Fig. 1]. The program performs pattern-based searches of databases, and displays discovered pattern results [See Table 2 and 4], and therefore inherently meets claims language for storing generated entries. Search results are tracked according to exact matches, matches within varying degrees of accuracy, and unmatched data [Table 5].

Rigoutsos does not teach deleting each matching subsequence from the sequence where it is found, as in claims 14, 27, and 28.

Rigoutsos does not teach concatenating unmatched regions of sequences that remain after deleting each matching subsequence to form and store a backbone sequence, as in claims 14, 24, 27, and 28 (step vi).

Rigoutsos does not teach generating a first representation of the sequence responsive to the stored backbone sequence and at least a portion of the stored match- set data and presenting the represented sequence to a user of the computer system; wherein one of the subsequences is matched by a certain plurality of the replets and the method further includes, as in claims 14, 24, 27, and 28 (step vii).

Rigoutsos does not teach generating or receiving a selection of one of the certain plurality of replets, wherein generating the first representation in step vii) is responsive to the selected one of the certain plurality of replets but not responsive to any non-selected replet, and wherein the selected one of the replets has a position within the sequence, and wherein after receiving the selection the computer system updates the first and second parameters for any non-selected replet associated with the selected one of the replets, the updating being responsive to the position of the selected one of the replets, as in claims 14, 24, 27, and 28 (step viii).

Rigoutsos does not teach generating or receiving a selection of a replet that was not selected in step viii); and generating and presenting a second representation of the sequence, wherein the representation in step x) is responsive to the one of the replets indicated by the selection in step ix) instead of the one of the replets indicated by the selection in step viii) and wherein the computer system performs the generating in step x) by reference to the first and second parameters for the one of the replets indicated by the selection in step ix), such that the computer system performs the generating in step x) using the position parameters updated in step viii), as in claims 14, 24, 27, and 28 (steps ix and x).

Chen teaches a program for identifying repeats in long DNA sequences [Introduction]. In particular, the program extracts repeats and concatenates regions (other that repeats) and sends the string as input to another program [p.1697, Col. 2, p.1698, Col. 1, and Fig. 1]. The program allows for encoding of repeat regions in the DNA sequences [p.1696-97, Methods]. This program is beneficial for improving search results through sequence compression [Introduction].

Orcutt teaches a nucleic acid sequence database computer system and program [Fig. 1]. The user can extract and concatenate any of the stored sequences, the complement, or the protein translations [p.168]. Sequences can be stored and examined by other matching programs [p.168]. The system provides functionality for updating the database files by adding or deleting any sequence entries [p.168]. The system contains print functions for displaying the contents of any file [p.165]. The system provides match functions for determining sequence matches and mismatches program, and outputs a representation of a sequence in response to a matching program that considers contiguous residues that match [p.164, last ¶, p.167]. The system will also search and identify nonexact matches [p.165], which meets claim language for non-selected replets.

Zhang teaches a computer-based method for identifying and graphically displaying repeat regions on a gene [Abstract, Fig. 1]. The program also displays gaps, mismatches (i.e. non-matching) regions, gaps, and multiple alignments [Fig. 2, Fig. 3]. The program interface also allows for searching a database and using filtering commands [Fig. 6], which inherently functions to remove data from a viewable data set (i.e. deletion). The program is beneficial for creating user friendly interpretation for viewing results when matching database sequences [Abstract].

UK CROPNET teaches a computer based method for graphically displaying sequences from a database. In particular, the generated displays include a combination of different sequence information including BLAST matches to an insert sequence, homology matches to an insert sequence, intron, exons, textual information [See pages 2-3]. Additionally, graphs are generated to include representations of physical positions of a probe in a region of a chromosome, backbone markers, and specific sequence information [p.4].

It would have been obvious to someone of ordinary skill in the art at the time of the instant invention to modify the method of Rigoutsos by deleting each matching subsequence from the sequence where it is found, and concatenating unmatched regions of sequences that remain after deleting each

matching subsequence to form and store a backbone sequence, as in claims 14, 24, 27, and 28, since Chen teaches a program that extracts repeats from a sequence and concatenates regions (other than repeats) for analysis by another program [p.1697, Col. 2, p.1698, Col. 1, and Fig. 1], and since Orcutt teaches a nucleic acid sequence database computer system and program wherein the user can perform sequence matching functions, deletion functions, and concatenation function for any of the stored sequences, as set forth above. The motivation would have been to improve the process of collecting, updating, and reviewing the abundance of published sequence data, as suggested by Orcutt [p.157], or to improve search results through sequence compression, as shown by Chen [Introduction].

It would have been obvious to someone of ordinary skill in the art at the time of the instant invention to modify the method of Rigoutsos does not teach generating a first representation of the sequence responsive to the stored backbone sequence and at least a portion of the stored match-set data, wherein one of the subsequences is matched by a certain plurality of the replets and the method further includes, as in claims 14, 24, 27, and 28 (step vii), since Orcutt provides software for displaying and updating any of the matched or unmatched data sets, as shown above, and since Zhang teaches a computer-based method for identifying and graphically displaying repeat regions, gaps, mismatches (i.e. non-matching) regions, and multiple alignments, as set forth above. The motivation would have been to improve sequence analysis using a user friendly program for viewing results when matching database sequences, as set forth above Zhang.

It would have been obvious to someone of ordinary skill in the art at the time of the instant invention to modify the method of Rigoutsos does not teach generating or receiving a selection of one of the certain plurality of replets, wherein generating the first representation in step vii) is responsive to the selected one of the certain plurality of replets but not responsive to any non-selected replet, and wherein the selected one of the replets has a position within the sequence, since Orcutt provides software for displaying and updating any of the matched or unmatched data sets, as shown above, and since Zhang

teaches a computer-based method for identifying and graphically displaying repeat regions, gaps, mismatches (i.e. non-matching) regions, and multiple alignments, as set forth above, and is capable of performing automated updates of annotation information [p.654, Col. 1]. The motivation would have been to improve sequence analysis using a user friendly program for viewing results when matching database sequences, as set forth above Zhang.

Rigoutsos does not teach generating or receiving a selection of a replet that was not selected in step viii); and generating and presenting a second representation of the sequence, wherein the representation in step x) is responsive to the one of the replets indicated by the selection in step ix) instead of the one of the replets indicated by the selection in step viii) and wherein the computer system performs the generating in step x) by reference to the first and second parameters for the one of the replets indicated by the selection in step ix), such that the computer system performs the generating in step x) using the position parameters updated in step viii), as in claims 14, 24, 27, and 28 (steps ix and x), since UK CROPNET teaches a computer based method for graphically displaying sequences using a combination of different sequence information including BLAST matches to an insert sequence, homology matches to an insert sequence, intron, exons, textual information, and backbone markers, as set forth above, and since Zhang teaches a computer-based method for identifying and graphically displaying repeat regions, gaps, mismatches (i.e. non-matching) regions, and multiple alignments, as set forth above, and specifically includes positional parameters [See Fig. 3, 4]. The motivation would have been to improve sequence analysis using a user friendly program for viewing results when matching database sequences, as set forth above Zhang.

Claims 3-6, 10, 14-22, 24-28 are rejected under 35 U.S.C. 103(a) as being unpatentable over Rigoutsos et al. (Bioinformatics, 1998, Vol. 14, No. 1, p. 55-67), in view of Chen et al. (Bioinformatics, 2002, Vol. 18, No. 12, p.1696-1698), in view of Orcutt et al. (Nucleic Acids Research, 1982, Vol. 10, No. 1, p. 157-174),

in view of Zhang et al. (Genome Research, 1997, Vol. 7, p.649-656), in view of UK CROPNETT (http://ukcrop.net/agr/sequence_display_key#sequence; Published 2001, p.1-5), and in view of Martinez et al. (Nucleic Acids Research, 1983, Vol. 11, No. 13, p. 4629-4634).

Rigoutsos, Chen, Orcutt, Zhang, and UK CROPNET make obvious the method, system, and computer readable medium of claims 4, 5, 14-22, 24, 27, and 28, as set forth above.

Rigoutsos, Chen, Orcutt, Zhang, and UK CROPNET do not teach storing information in a table using a "pointer", as in claims 3, 6, and 25.

Rigoutsos, Chen, Orcutt, Zhang, and UK CROPNET do not specifically teach storing multiple views of the sequence data at multiple levels of abstraction, as in claim 10. However, this limitation would have been obvious to one of ordinary skill in the art at the time of the invention since both Zhang and UK CROPNET teach computer programs that are capable of graphically displaying sequence data comprising various types of data and since UK CROPNET teaches using different graphical schemes for distinguishing between the different types of data present (e.g. different colors), as set forth above, which reasonably suggests the claimed limitation. The motivation would have been to improve sequence analysis using a user friendly program for viewing results when matching database sequences, as set forth above Zhang.

Martinez teaches a computer program for finding repeats in molecular sequences using pointers to indicate order and variation between sequences [Abstract and p.4630].

It would have been obvious to someone of ordinary skill in the art at the time of the instant invention to modify the method, system, and computer readable media made obvious by Rigoutsos, Chen, Orcutt, Zhang, and UK CROPNET by storing pointer information, as in claims 3 and 6, since Martinez teaches a computer program for finding repeats in molecular sequences using pointers to indicate order and variation between sequences, as shown above. The motivation would have been to improve sorting of

repeat sequences using a program designed to handle large sequences, as shown by Martinez [p.4630, 4634].

Response to Arguments

Applicant's arguments filed 05/11/2009 that the combination of Taylor, Schwartz, and Huysmans do not teach for each replet, a match-set data structure comprising a sequence identification to identify a subsequence where a match occurs and offset information to determine a position within the sequence where the matching subsequence of the sequence is located, wherein the offset information comprises a first and second position parameter, the first position parameter denoting a location in the sequence and the second position parameter denoting an offset from the location" have been fully considered but are moot in view of the new grounds of rejections.

Conclusion

Any inquiry concerning this communication or earlier communications from the examiner should be directed to Pablo Whaley whose telephone number is (571)272-4425. The examiner can normally be reached between 12pm-8pm.

If attempts to reach the examiner by telephone are unsuccessful, the examiner's supervisor, Marjorie Moran can be reached at 571-272-0720. The fax phone number for the organization where this application or proceeding is assigned is 571-273-8300.

Information regarding the status of an application may be obtained from the Patent Application Information Retrieval (PAIR) system. Status information for published applications may be obtained from either Private PAIR or Public PAIR. Status information for unpublished applications is available through Private PAIR only. For more information about the PAIR system, see http://pair-direct.uspto.gov. Should you have questions on access to the Private PAIR system, contact the Electronic Business Center (EBC) at 866-217-9197 (toll-free).

Pablo S. Whaley

Patent Examiner

Art Unit 1631

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